85. The variant allele of claim 84 wherein said variant allele is isolated.

86. The isolated variant allele of Claim 85, detectably labeled.

87. An isolated nucleic acid molecule selectively hybridizable to the isolated variant allele of Claim 85.

88. The isolated nucleic acid molecule of Claim 87, detectably labeled.

89. A variant allele of a human mu opioid receptor gene which encodes a variant human mu opioid receptor comprising an amino acid sequence having a variation in SEQ ID NO:2, wherein said variation comprises Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly 63.

90. The variant allele of claim 89 wherein said variant allele is isolated.

91. A isolated variant human mu opioid receptor comprising an amino acid sequence having a variation in SEQ ID NO:2, wherein said variation comprises Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly 63.

92. An antibody having a variant human mu opioid receptor of Claim 91 as an immunogen.

93. The antibody of Claim 92, detectably labeled

94. A cloning or expression vector comprising an isolated variant allele of a human mu opioid

receptor gene and an origin of replication, wherein said variant allele comprises a DNA of claim 84.

95. A cloning or expression vector comprising an origin of replication and an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene, wherein said variant allele comprises a DNA sequence of claim 84.

96. An expression vector comprising an isolated variant allele of a human mu opioid receptor gene comprising a DNA sequence of claim 84.

97. An expression vector comprising an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene, wherein said isolated nucleic acid molecule is operatively associated with a promoter, and said variant allele comprises a DNA sequence of claim 84.

98. A unicellular host transformed or transfected with an expression vector comprising an isolated variant allele of a human mu opioid receptor gene operatively associated with a promoter, wherein said variant allele comprises a DNA sequence of claim 84.

99. A unicellular host transformed with an expression vector comprising an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene, wherein said isolated nucleic acid molecule is operatively associated with a promoter, and said variant allele comprises a DNA sequence of claim 84.

100. An isolated variant allele of a human mu opioid receptor gene, wherein said variant allele comprises a DNA sequence of claim 84 having at least two variations in SEQ ID NO:1, wherein said variations comprise T67C; T124A; C153T; G174A or 187INS:GGC.

101. The isolated variant allele of Claim 100 detectably labeled.

102. An isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene comprising a DNA sequence of claim 84 having at least two variations in SEQ ID NO:1.

103. The isolated nucleic acid molecule of Claim 102, detectably labeled.

104. An isolated variant allele of a human mu opioid receptor gene, which encodes a variant human mu opioid receptor comprising an amino acid sequence having at least two variations in SEQ ID NO:2, wherein at least one said variation comprises Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly63.

105. An isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene of claim 84, wherein and said variant allele comprises a DNA sequence having at least two variations in SEQ ID NO:1, and at least one of said variations comprises T67C; T124A; C153T; G174A or 187INS:GGC, so that said isolated nucleic acid molecule encodes a variant human mu opioid receptor comprising at least two variations in sequence of SEQ ID NO:2, wherein at least one of said variations comprises Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly63.

106. A variant human mu opioid receptor of claim 91 comprising an amino acid sequence having at least two variations in SEQ ID NO:2, wherein at least one of said variations comprises Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly63.

107. An antibody having a variant human mu opioid receptor of Claim 106 as an immunogen.

108. The antibody of Claim 107, detectably labeled.

109. A cloning or expression vector comprising an isolated variant allele of a human mu opioid receptor gene and an origin of replication, wherein said variant allele comprises a DNA sequence of claim 84 having at least two variations in SEQ ID NO:1, wherein at least one of said variations comprises T67C; T124A; C153T; G174A; or 187INS:GGC.

110. A cloning or expression vector comprising an origin of replication and an isolated nucleic acid molecule selectively hybridizable to an isolated variant allele of a human mu opioid receptor gene, wherein said variant allele comprises a DNA sequence of claim 84 having at least two variations in SEQ ID NO:1, wherein at least one of said variations comprises T67C; T124A; C153T; G174A; or 187INS:GGC.

111. A unicellular host transformed with an expression vector of Claim 109.

112. A unicellular host transformed with an expression vector of Claim 110.

113. A method for determining a susceptibility in a subject to at least one addictive disease,

comprising the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene;

b) determining whether said human mu opioid receptor gene of said first allele comprises a DNA sequence of claim 84,

such that the presence of said at least one variation in said human mu opioid receptor gene of said first allele is expected to be indicative of the subject's susceptibility to at least one addictive disease relative to the susceptibility to said at least one addictive disease in a standard.

114. The method for determining a susceptibility to at least one addictive disease of Claim 113, further comprising the step of determining whether said human mu opioid receptor gene of said second allele comprises a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C; T124A; or 187INS:GGC, such that the presence of said at least one variation in said human mu opioid receptor gene of said second allele is expected to be indicative of the subject's susceptibility to said at least one addictive disease relative to the susceptibility to said at least one addictive disease in said standard.

115. The method of either of Claim 114 wherein said at least one addictive disease comprises opioid addiction; cocaine addiction or addiction to other psychostimulants; nicotine addiction; barbituate or sedative hypnotic addiction; anxiolytic addiction; or alcohol addiction.

116. A method for determining a susceptibility to at least one addictive disease in a subject relative to susceptibility in a standard, comprising the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a human mu

opioid receptor;

b) determining whether said human mu opioid receptor comprises an amino acid sequence of claim 91,

such that the presence of said at least one variation is expected to be indicative of the susceptibility to said at least one addictive disease in said subject relative to susceptibility to said at least one addictive disease in said standard, wherein the human mu opioid receptor of said standard comprises an amino acid sequence of SEQ ID NO:2.

117. The method of Claim 116, wherein said at least one addictive disease comprises opioid addiction; cocaine addiction or addiction to other psychostimulants; nicotine addiction; barbituate or sedative hypnotic addiction; anxiolytic addiction; or alcohol addiction.

118. A method for determining a susceptibility to pain in a subject relative to a susceptibility of pain in a standard, wherein the method comprises the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene;

b) determining whether said human mu opioid receptor gene of said first allele comprises a DNA sequence of claim 84,

such that the presence of said at least one variation in said human mu opioid receptor gene of said first allele is expected to be indicative of susceptibility to pain in said subject relative to susceptibility to pain in said standard, wherein said first allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

119. The method of Claim 118 for determining a susceptibility to pain in a subject, further comprising

the step of determining whether said second allele of said bodily sample comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C, T124A or 187INS:GGC, such that the presence of said at least one variation in said second allele is expected to be indicative of susceptibility to pain in said subject relative to susceptibility of pain in said standard, wherein said second allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

120. A method for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in said subject relative to a therapeutically effective amount of pain reliever to administer to a standard in order to induce analgesia in said standard, wherein the method comprises determining a susceptibility to pain in said subject relative to susceptibility to pain in said standard, wherein susceptibility to pain in said subject is expected to be indicative of said therapeutically effective amount of pain reliever to administer to said subject to induce analgesia in said subject relative to said therapeutically effective amount of pain reliever to administer to said standard to induce analgesia in said standard.

121. The method of Claim 120 for determining a therapeutically effective amount of pain reliever to administer to said subject, wherein determining susceptibility to pain in said subject comprises the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene; and

b) determining whether said first allele comprises a human mu opioid receptor gene comprising a DNA sequence having a variation in SEQ ID NO:1, wherein said variation

comprises T67C; T124A; C153T; G174A or 187INS:GGC, or combinations thereof, wherein the presence of said at least one variation in said human mu opioid receptor gene of said first allele is expected to be indicative of the subject's susceptibility to pain relative to said to susceptibility of pain in said standard, wherein said first allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1, such that said therapeutically effective amount of pain reliever to administer to the subject in order to induce analgesia is related to said susceptibility to pain in said subject relative to susceptibility to pain in said standard.

122. The method of Claim 121, wherein determining susceptibility to pain in said subject relative to susceptibility to pain in said standard further comprises the step of determining whether said second allele of said bodily sample from said subject comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said at least one variation comprises T67C, T124A or 187INS:GGC, such that the presence of said at least one variation in said second allele is expected to be indicative of susceptibility to pain in said subject relative to susceptibility to pain in said standard, wherein said second allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1, and the therapeutically effective amount of pain reliever to administer to said subject to induce analgesia in said subject is related to the presence of said at least one variation in said human mu opioid receptor gene of said second allele of said bodily sample from said subject.

123. A method for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease in said subject relative to a therapeutically effective amount of therapeutic agent to administer to

a standard suffering from the at least one addictive disease to treat the at least one addictive disease in said standard, wherein the method comprises the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene; and

b) determining whether said first allele comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C, T124A or 187INS:GGC,

wherein the presence of said at least one variation in said human mu opioid receptor gene of said first allele is expected to be indicative of the therapeutically effective amount of said therapeutic agent to administer to the subject to treat said at least one addictive disease in said subject relative to said therapeutically effective amount of said therapeutic agent to administer to said standard to treat said at least one addictive disease in said standard, wherein said first allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

124. The method of Claim 123 for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from said at least one addictive disease to treat said at least one addictive disease, relative to said therapeutically effective amount of said therapeutic agent administered to said standard suffering from said at least one addictive disease to treat said at least one addictive disease in said standard, further comprising the step of determining whether said second allele of said bodily sample from said subject comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C; T124A; or 187INS:GGC, such that the presence of said at least one variation in said second allele related to said therapeutically effective amount of said therapeutic

agent administered to said subject to treat said at least one addictive disease in said subject relative to said therapeutically effective amount of said therapeutic agent to administer to said standard to treat said at least one addictive disease in said standard, wherein said second allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

125. The method of either of Claims 123 or 124, wherein said at least one addictive disease comprises opioid addiction; cocaine addiction or addiction to other psychostimulants; nicotine addiction; barbiturate or sedative hypnotic addiction; anxiolytic addiction; or alcohol addiction.

126. A commercial test kit may for determining the presence of at least one variation in a human mu opioid receptor gene of an allele in a bodily sample taken from a subject, wherein the commercial test kit comprises:

a) PCR oligonucleotide primers suitable for detection of an allele comprising a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1 comprising T67C; T124A; C153T; G174A; or 187INS:GGC;

b) other reagents; and

c) directions for use of the kit.

127. A commercial test kit for detecting a variant human mu opioid receptor in a bodily sample taken from a subject, comprising

(a) predetermined amount of at least one detectably labeled immunochemically reactive component having affinity for a variant human mu opioid receptor; said variant being at least one of Ser23Pro, Ser42Thr or the addition of a Gly residue following Gly 63;

(b) other reagents; and

(c) directions for use of the kit.

128. A commercial test kit for detecting a variant human mu opioid receptor in a bodily sample taken from a subject, wherein said kit comprises:

(a) a labeled component which has been obtained by coupling the human mu opioid receptor of the bodily sample to a detectable label;

(b) one or more additional immunochemical reagents of which at least one reagent is a ligand or an immobilized ligand, which ligand comprises:

(i) a ligand capable of binding with the labeled component (a);

(ii) a ligand capable of binding with a binding partner of the labeled component (a);

(iii) a ligand capable of binding with at least one of the component(s) to be determined; or

(iv) a ligand capable of binding with at least one of the binding partners of at least one of the component(s) to be determined;

(c) directions for the performance of a protocol for the detection and/or determination of one or more components of an immunochemical reaction between the human mu opioid receptor and a specific binding partner thereto.

129. A method for diagnosing a disease or disorder related to a physiological function regulated by the hypothalamus pituitary adrenal axis (HPA) or the hypothalamus pituitary gonadal axis (HPG), wherein the method comprises the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene;

b) determining whether said human mu opioid receptor gene of said first allele comprises a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C; T124A; or 187INS:GGC,

such that the presence of said at least one variation in said human mu opioid receptor gene of said first allele is expected to be indicative of a disease or disorder related to a physiological function regulated by the hypothalamus pituitary adrenal axis (HPA) or the hypothalamus pituitary gonadal axis (HPG), wherein said first allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

130. The method of Claim 129, wherein said physiological function comprises sexual or reproductive function, gastrointestinal motility, immune response, or ability to withstand stress.

131. The method of Claim 130, wherein said disease or disorder comprises infertility, constipation, diarrhea, decreased immune response relative to said standard, or decreased ability to withstand stress relative to said standard.

132. The method of Claim 130 for diagnosing a disease or disorder related to a physiological function regulated by the HPA or HPG, further comprising the step of determining whether said second allele of said bodily sample comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said variation comprises T67C; T124A; or 187INS:GGC, such that the presence of said at least one variation in said second allele is expected to be indicative of a disease or disorder related to a physiological function regulated by the HPA or HPG axes, wherein said second allele of said standard comprises a human mu opioid receptor gene comprising a DNA sequence of SEQ ID NO:1.

133. The method of Claim 132, wherein said physiological function comprises sexual or reproductive function, gastrointestinal motility, immune response, or ability to withstand stress.

134. The method of Claim 132, wherein said disease or disorder comprises infertility, constipation, diarrhea, decreased immune response relative to said standard, or decreased ability to withstand stress relative to said standard.

135. The method of Claim 132, wherein said disease or disorder comprises diarrhea.

136. A method for selecting an appropriate therapeutic agent and a therapeutically effective amount of said agent to administer to said subject to treating a disease or disorder related to a physiological function regulated by the HPA or HPG axes, wherein the method comprises diagnosing said disease or disorder in said subject, wherein said disease or disorder is expected to be indicative of said appropriate therapeutic agent for treating said disease or disorder.

137. The method of Claim 136, wherein said physiological function comprises reproductive or sexual function, gastrointestinal motility, immune response, or ability to withstand stress.

138. The method of Claim 136, wherein diagnosing said disease or disorder in said subject comprises the steps of:

a) removing a bodily sample from said subject, wherein said sample comprises a first and second allele comprising a human mu opioid receptor gene; and

b) determining whether said first allele comprises a human mu opioid receptor gene comprising a DNA sequence having at least one variation in SEQ ID NO:1, wherein said